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Sequence
Strd Orig ZScore EScore Len | Documentation | Gen220 Sig | Gen226 | Strd Orig ZScore | Escore Len | Documentation | Gen221 | Gen226 | Strd Orig ZScore | Escore Len | Documentation | Gen226 | Strd Orig ZScore | Strd Orig ZScor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "MODEL-frame+ n2p.model -DEV=xlp
-0-/cgn2_1/USPTO_spool/6228611/runat_28082002_100210_13561/app_query.fasta_1.1639
-0-/cgn2_1/USPTO_spool/6228611/runat_28082002_100210_13561/app_query.fasta_1.06-Cgn2_1/USPTO_spool/6228611/runat_28082002_100210_13561/app_query.fasta_1.1639
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPEXT=0.000 -GARPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS-humman40.cdi -LIST=45 -DOCALIGN=0.000 -THR_SCORE=pct
-NORM-ext -HEADSIZE=500 -MINIEN=0 -MAXIEN=2000000000
-USER=6228611_0CGN1_1.54 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XIEVX -WAIT -THREADS=1
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5.3e-19
5.3e-19
3.6e-18
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91.00 416.91 2.9e-16
281.00 401.05 2.0e-1
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480.09
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465.18
OM of: US-08-711-417C-165 to: Issued_Patents_AA:* out_format : pfs
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                                                                                                                                                                                                                                                        About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:05-09-234-613-14 + 28
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:05-08-486-099-117 + 26
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:05-08-860-107A-127 + 26
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:05-08-8618-223B-117 + 26
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/cgn2_6/ptodata/2/1aa/6A_COMB.pep:US-08-475-668-117 +
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:US-08-485-551A-117 +
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Database sequences: 211528
Database length: 24425594
Search time (sec): 34.160000
                                                                                                                               Date: Aug 28, 2002 10:02 AM
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Query length: 1551
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356.77 4.7e-13
356.77 4.7e-13
356.77 4.7e-13
/cgn2_6/ptcdata/2/iaa/6A_COMB.pep:US-08-471-913A-117 + 253.00 356.77 4.7e-/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:US-08-478-264A-117 + 253.00 356.77 4.7e-/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:US-08-474-349A-117 + 253.00 356.77 4.7e-/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:US-08-474-349A-117 + 253.00 356.77 4.7e-/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:US-09-063-035-2 + 251.50 348.40 7.9e-13/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:US-08-475-844-5 + 248.50 345.02 1.4e-12
                                                                                                                                                                                                                                                                     APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
                                                                                                                                  seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-711-417C-202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 5.329 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/711,417C
                                                                                                                                                                                                                                                                                                                                                                   "ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAX-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 202:
                                                                                                                                                                                                        Sequence 202, Application US/08711417C Patent No. 6228611 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-711-417C-165 x US-08-711-417C-202
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 516 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 202: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
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Ratio: 5.329
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951 CATCAACTACCTGGGGGCCGAGTCCCTGCGCCCGCTGGTGCAGACGCCCC 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        901 GAGAACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 851 GGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAAG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 lyThrLeuTyrProVall1eLysGluGluThrLysHisSerGluMetAla 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTCGTGCTGGACAGACT 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801 AGCAAGTAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701 GCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 CACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGA 650'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 HislysCysGlyTyrCysGlyArgSerTyrLysGlnArgThrSerLeuGl 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651 GGAACATAAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGG 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 TICCGGGGGAGAAGCCCTTCAAATGCCACCTCTGCAACTACGCCTGCCGCC 550
                                                                                                                                                                                                                                                                                                                                                                                     551 GGAGGGACGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600
                                                                                                                                                                                                                                                                                401 ITCACAAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGC 450
                                                                                                                                                                                                                                                                                            301 AGCTCGGCTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACT 350
                                                                                                                                                                                                  351 AAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGG 400
                                                                                                                                                                                                                                              251 IGCTIGATGCCICGGGAGAGAAATGAATGGCTCCCACAGGGACCAAGGC 300
                                                                                            201 TGGGCGTGCCTGTGAATGAATGGGGGAAGAATGTGCGGAGGATTTACGAA 250
                                              151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA 200
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APPLICANT: Georgopoulos, Katia A. TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1401 CTTCCTGGATCACGTCATGTACACCATCCACATGGGCTGCCACGGCTTCC 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                  1351 ACCAGCGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCGGGTGCT 1400
                                                                                                                                                                                                                                                                                                             1251 CCGACGCGCGAACGCGTGTCGCTCAAGGAGGAGCACCGCGCGCTACGACC 1300
                                                                                                                                                                                                                                                                                                                                                                        1301 TGCTGCGCGCCTCCGAGACTCGCAGGACGCGCTCCGCGTGGTCAGC 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1101 CGTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGGAGC 1150
                                                                                                                                                                                      1151 GCGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAGAGC 1200
                                                                                                                                                                                                                                                                                                                                                                                         451 ThrSerGlyGluGlnMetLysValTyrLysCysGluHisCysArgValle 467
                                                                                                                                                                                                                                                                1501 GAGTICICGICGCACAIAACGCGAGGGGAGCACCGCIICCACAIGAGC 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-711-417C-196
                                                                                                                                                                                                                  384 rgGlualaSerProSerAsnSerCysGlnAspSerThrAspThrGluSer 400
                                                                                                                                            COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTWARE: PASTERO for Windows 95
SOFTWARE: PASTERO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/213,438
FILING DATE: 14-SEP-1993
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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MEDIUM TYPE: Diskette
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ZIP: 02110-2804
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615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 AATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAATGGGCGTGCCTGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 AATGAATGGGGAAGAATGTGCGGAGGATTTACGAATGCTTGATGCCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGAGAAAATGAATGCCTCCCACAGGGACCAAGGCAGCTCGGCTTTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 TGGGATCATTTGCATCGGGCCCAATGTGCTCATGGTTCACAAAAGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 ACACTGGAGAACGCCCCTTCCAGTGCAATCAGTGCGGGGCCTCATTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516 CTTCAAATGCCACCTCTGCAACTACGCCTGCCGCCGGAGGGACGCCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      566 CTGGCCACCTGAGGACGCACTCCGTTGGTAAACCTCACAAATGTGGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           616 TGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGAGAGGAACATAAAGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAspIleCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   466 CAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 461
                                                  NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 196:
APPLICATION NUMBER: 07/946,233 FILING DATE: 14-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-711-417C-165 x US-08-711-417C-196
                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: US-08-711-417C-196
                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO: 196:
SEQUENCE CHARACTERIFICS:
LENGTH: 461 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 5.351
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                        Quality: 2467.00
                                                                                                                                                                                                                                                                                                       US-08-711-417C-196
                                                                                                                                                                                                                                                                                                                                                          alignment_scores
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                                                    267 yAlaGluSerLeuArgProLeuValGlnThrProProGlyGlySerGluV 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 alvalprovalileSerprometTyrGlnLeuHisArqArqSerGluGly
167 gCysHisAsnTyrLeuGluSerMetGlyLeuProGlyThrLeuTyrProV
                                                                                                                                                                                                                                                   CCGACACGCCCTACGACAGTGCCACGTACGAGAAGGAGAACGAAATGATG
                                                                                                                                                                                                                                                                      317 uLeuLeuSerLysAlaLysLeuValProSerGluArgGluAlaSerProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 MetLysValTyrLysCysGluHisCysArgValLeuPheLeuAspHisVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 ysAsnMetCysGlyTyrHisSerGlnAspArgTyrGluPheSerSerHis
                                                                                                        ATAGGATCAGAGAGATCTCTCGTGCTGGACAGACTAGCAAGTAATGTCGC
                                                                                                                          CAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGGGCCTGT
                                                                                                                                                                                               AAGTCCCACGTGATGGACCAAGCCATCAACAACGCCATCAACTACCTGGG
                                                                                                                                                                                                                                                                                                                                                                                             GGCCGAGTCCCTGCGCCGCTGGTGCAGACGCCCCCGGGCGGTTCCGAGG
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seg_documentation_block:

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Sequence 198, Application US/08711417C
Patent No. 6228611
GENERAL INFORMATION:
APPLICANT GEOTOPOULOS, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 CCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAAGCTCCAAGAGTGAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 CCCCCCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGATCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSED for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 518
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                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 10287/007001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQUENCE DESCRIPTION: SEQ ID NO: 198: US-08-711-417C-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Myers, Louis P. REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-711-417C-165 x US-08-711-417C-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-711-417C-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 518 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 198: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouality: 2437.00
Ratio: 4.913
Percent Similarity: 95.202
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                                                                                                                                                                                                          CITY: Boston STATE: MA
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CATCAACTACCTGGGGGCCGAGTCCCTGCGCCCGCTGGTGCAGACGCCCC 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1098 CGCCGTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGG 1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AGCTCGGCTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACT 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAsnAl 315
                                                              251 TGCTTGATGCCTCGGGAGAGAAATGAATGGCTCCCACAGGGACCAAGGC 300
                                                                                                                                               351 AAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGG 400
                                                                                                                                                                                                               TTCACAAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGC 450
                                                                                                                                                                                                                                                                                                                                                184
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGGGACGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600
201 TGGGCGTGCCTGTGAAATGAATGGGGAAGAATGTGCGGAGGATTTACGAA 250
                                                                                                                                                                                                                                                                                                                             GGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                               501 TICCGGGGAGAAGCCCTICAAATGCCACCTCTGCAACTACGCCTGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTCGTGCTGGACAGACT
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                 GGAACATAAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGG
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Ratio:

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APPLICANT:
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 152
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                          1435
                                                                                                                                                                                                                                                                     1344
                                   1148 AGCGCGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAG 1197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1486 AGCCAGGACCGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCG 1535
                                                                                                              1345 GTCAGCACCAGCGGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCG 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1436 GCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCAC 1485
                                                   381 luargGlualaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 397
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365 .AlaValAspAsnLeuLeuLeuLeuSerLysAlaLysSerValSerSerG 381
                                                                                                                                                                                                                1395 GGTGCTCTTCCTGGATCACGTCATGTACACCATCCACATG.......G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisAr
                                                                                                                                1295 ACGACCTGCTGCGCCCCTCCGAGAACTCGCAGGACGCGCTCCGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                          1248 CGCCCGACGCGCGCAACGC...GTGTCGCTCAAGGAGGAGCACCGCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 946,233
FILING DATE: 14-SEP-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 568 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1536 CTTCCACATGAGC 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-08743-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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571

Length:

Quality: 2422.00

alignment_scores:

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51 CCCCCCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGATCC 100
                                                                                                                                                                                                                                                                               101 CCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAAAGCTCCAAGAGTGAC 150
                                                                                                                                                                                                                                                                                                                                                  151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGCGTGCCTGTGAATGAATGGGGGAAGAATGTGCGGGAGGATTTACGAA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGCITGATGCCTCGGGAGAGAAATGAATGGCTCCCACAGGGACCAAGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnCys 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICACAAAAGAAGCCACACIGGAGAACGGCCCTICCAGIGCAAICAGIGC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGGGACGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuGl 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  651 GGAACATAAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGG 700
                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                     etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 AGCTCGGCTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 7
Percent Identity: 82.137
                                                                                                     Align seg 1/1 to: PCT-US93-08743-5 from: 1. to: 568
                                                  alignment_block:
US-08-711-417C-165 x PCT-US93-08743-5
4.863
87.215
                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
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564 gTyrHisLeuSer 568

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951 CATCAACTACCTGGGGGCCGGGTCCCTGCGCCGCTGGTGCAGACGCCCC 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1436 GCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCAC 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1486 AGCCAGGACCGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCG 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1001 CGGGCGGTTCCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1051 AGG. .. CGCTCGGAGGGCACCCCGCGCTCCAACCACTCGGCCCAGGACAG 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1098 CGCCGTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGG 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1148 AGCGCGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1295 ACGACCTGCTGCGCGCCGCCTCCGAGAACTCGCAGGACGCGCTCCGCGTG 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1248 CGCCCGACGCGCGCAACGC...GTGTCGCTCAAGGAGGAGCACCGCGCCT 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1345 GTCAGCACCAGCGGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCG 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498 ValSerThrSerGlyGluGlnLeuLysValTyrLySCluHisCysAr 514
                                                                                                                                                                                                                                                                                                                                                                                                                         901 GAGAACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 alleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIl 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 316
                                                                                                                                                                                                                                                                                                                   316 uAlaSerAsnValAlaLySArgLySSerSerMetProGlnLySPheLeuG 333
                                                                                                                                                                                                                                                                                                                                                                                           851 GGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAAG 900
267 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 284
                                                                                                                              284 ly...MetTyrProValIleLysGluGluThrAsnHisAsnGluMetAla 299
                                                                                                                                                                                  751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTCGTGCTGGACAGACT 800
                                                                                                                                                                                                                                                                                        801 ACCAAGTAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        701 GCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCA
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Sequence 153 Application US/08465590

Patent No. 5824770

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TILLE OF INVENTION: IRANOS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAATGGGCGTGC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 CTGTGAAATGAATGGGGAAGAATGTGCGGAGGATTTACGAATGCTTGATG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 CCTCGGGAGAGAAATGAATGGCTCCCACAGGGACCAAGGCAGCTCGGCT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AlaSerAsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:U$-08-465-590-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 90.385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-465-590-153 from: 1 to: 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
FILING DATE: 05-JUN-1994
PRICH APPLICATION NUMBER: US 08/238,212
FILING DATE: 10-SPE-1994
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SPE-1993
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-193
ATTORNEY/AGENT INFORMATION:
NAME: MAPER 11 NFORMATION:
NAME: NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-711-417C-165 x US-08-465-590-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: MPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 153:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 2207.50
Ratio: 5.098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MASSACHUCETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 92.521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: 1
STATE:
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31(SerGlyGluLysMetasnGlySerHisArgaspGlnGlySerSeral 3TCGGGAGTTGGAGCATTCGACTTCCTAACGGAAAACTAAAGTGTG	2 5
53		0
360	<pre>0 TAICTGTGGGATCATTTGCATCGGCCCAATGTGCTCATGGTTCACAAA 4</pre>	60
410	GAAGCCACACTGGAGAACGCCCTTCCAGTGCAATCAGTGCGGGGCCTCA 4	59
460	TTCACCCAGAAGGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGGA 5	09 19
510 119	GAAGCCCTTCAAATGCCACTCTGCAACTACGCCTGCCGCCGGGGGGGC 5.	59 36
560 136	CCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCTCACAAATGT 6	52
610 153	GGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGAGGAACATAA 6: 	69
169	AGAGGGGGCACACAACTAGGAAAGCATGGGCCTTCCGGGCACACTGT 7. 	60
7,10	ACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGACCTG 7	59
760 203	TGCAAGATAGGATCAGAGATCTCTCGTGCTGGACAGACTAGCAAGTAA 8:	09 19
810 219	TGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGG 8 	59
860 236	GCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAAGGAAG	09 52
910 253	ATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGCCATCAACTA 95 	69
960	CCTGGGGGCCGGGTCCCTGCGCCGCTGGTGCACGCCCCCGGGGGGTT 10 {	900
1010 286	CCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCACAGGCGC 10)56)2
303	TCGGAGGGCACCCGCGCTCCAACCACTCGGCCCAGGACAGCGCCGTGGA 11 	90:
319	GTACCTGCTGCTGCTCCCAAGGCCAAGTTGGTGCCCTCGGAGCGCGAGG 11	56
1157 336	CGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAGAGCAACAC 12 	906

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1257 CGCG...CAACGCGTGTCGCTCAAGGAGGAGCACCGCGCCTACGACCTGC 1303
                                                                                                                                                                          1304 TGCGCGCCGCCTCCGAGAACTCGCAGGACGCGCTCCGCGTGGTCAGCACC 1353
1207 GAGGAGCAGCGAGCGGTCTTATCTACCTGACCAACCACATCGCCCGACG 1256
                                                                                                                                                                                                                                                                                                                                             1404 CCTGGATCACGTCATGTACACCATCACATG......GGCTGCCACG 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                 1445 GCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGGCTACCACAGGCCAGGAC 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1495 CGGTACGAGTTCTCGTCGCACATAACGCGAGGGGGGGCACCGCTTCCACAT 1544
                             369 *Ala***********LeuLysGluGlu***ArgAlaTyr****1 386
                                                                                                                                                                                                453 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArg***His** 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08283300A
Patent No. 6172278
GENERAL INFORMATION:
APPLICANT: GEOTOPOPULOS, Katia A.
TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-283-300A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: MYGIS, PAUL L.
REGISTRATION NUMBER: 35,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII (LEXT)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,300A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MGP-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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710 ACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGACCTG 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 760 TGCAAGATAGGATCAGAGAGATCTCTCGTGCTGGACAGACTAGCAAGTAA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCACCCAGAAGGGCAACCTGCTCCGGCACATCCAAGCTGCATTCCGGGGA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 PheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGl 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGCCCTTCAAATGCCACCTCTGCAACTACGCCTGCCGCCGGAGGGACG 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           660 AGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCACACTGT 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 TIGICGGGAGIIGGAGGCATICGACTICCTAACGGAAAACTAAAGIGIGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 TATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCCATGGTTCACAAAA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCGGGAGAGAAATGAATGGCTCCCACAGGGACCAAGGCAGCTCGGCT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560 CCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCTCACAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 CIGTGAAATGAATGGGGAAGAATGTGCGGAGGATTTACGAATGCTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                   160 GCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAATGGGCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 LeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAs
                                                                                                                                                                                                                                                               Percent Identity: 90.385
                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-283-300A-13 from: 1 to: 470
                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-711-417C-165 x US-08-283-300A-13
INFORMATION FOR SEQ ID NO: 13:
               SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                           Quality: 2207.50
Ratio: 5.098
Percent Similarity: 92.521
                                                                                                                                                     US-08-283-300A-13
                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260
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seq_name: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:PCT-US95-09345-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1495 CGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCGCTTCCACAT 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1157 CGTCCCCGAGCAACAGGTGCCAAGACTCCACGACACCGAGGCCAACAC 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCACAGCCAGGAC 1494
                                                                                                                                                                                                                                                                                                                                                                        TCGGAGGGCACCCCGCGCTCCAACCACTCGGCCCAGGACAGCGCCGTGGA 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1107 GTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGGAGCGCGAGG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGAGCAGCGCTCTTATCTACCTGACCAACCACATCGCCCGACG 1256
                                                                                                                                                                                                                     CCTGGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACGCCCCGGGCGGTT 1009
                                                                                                                                                                                                                                                                                                1010 CCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC...AGGCGC 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 ****LeuLeuLeuLeuSerLysAlaLys***Val***SerGluArgGluA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 eLeuAspHisValMetTyrThrIleHisMet******GlyCysHisG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 erGluValValProValIleSerProMetTyrGlnLeuHis****** 302
                                                                                          910 ATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGCCATCAACTA 959
                                                                                                                                                                    860 GCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAAGGAGAACGAA 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 GluGluGlnArgSerGlyLeulleTyrLeuThrAsnHislle*****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              810 IGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1545 GAGC 1548
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160 GCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAATGGGCGTGC 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 TIGICGGGAGITGGAGGCATICGACTICCTAACGGAAAACTAAAGIGIGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATCIGIGGATCATITGCATCGGGCCCCAATGTGCTCATGGTTCACAAAA 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: PCT-US95-09345-13 from: 1 to: 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY AGENT INFORMATION:
ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                               SURTHARE: ASCII (LEXT)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09345
FILING DATE:
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/283,300 FILING DATE: 29-JULY-94 PRIOR APPLICATION DATA:
                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-711-417C-165 x PCT-US95-09345-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MGP-(TELECOMMUNICATION INFORMATION: TELEFAN: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Myers, Paul L. REGISTRATION NUMBER: 35,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 470 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                         STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 2207.50
Ratio: 5.098
nilarity: 92.521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                         BOSTON
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                                                                                              02109
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1010 CCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC...AGGCGC 1056
                                                                                           CCTGGGGGCCGAGTCCCTGCGCCCGCTGCAGACGCCCCCGGGCGGTT 1009
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                     610 GGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGAGGAACATAA 659
                                                                                                                                                                                                                                                                                                                                                                                                                                              710 ACCCAGTCATTAAAGAAGAACTAAGCACAGTGAAATGGCAGAAGACCTG 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                760 IGCAAGAIAGGAICAGAGAGAICICICGIGCIGGACAGACIAGCAAGIAA 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           910 ATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGCCATCAACTA 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 Ser***Gly***ProArgSerAsnHisSerAlaGlnAsp***AlaVal** 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    860 GCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAAGGAGAACGAA 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 ****LeuLeuLeuLeuSerLysAlaLys***Val***SerGluArgGluA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 GAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 ITCACCCAGAAGGCCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGGA
                                                                                                                                                                                                                   560 CCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCTCACAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 GluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIle******
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Sequence 153, Application US/08711417C
Patent No. 6228611
GENERAL INFORMATION:
APPLICANT: GENERACOPOULOS, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
1304 TGCGCGCCCCCCCGAGAACTCGCAGGACGCGCTCCGCGGGGTCAGCACC 1353
                                                                                                                                                                                                                                                                                                                                                                                    1495 CGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCGCTTCCACAT 1544
                                                                                              1354 AGCGGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCGGGTGCTCTT 1403
                                                                                                                                                                                             1404 CCTGGATCACGTCATGTACACCATCCACATG......GGCTGCCACG 1444
                                                                                                                                                                                                                                                                                          1445 GCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCACAGCCAGGAC 1494
                      403 SerGlyGluGln***LysValTyrLysCysGluHisCysArgValLeuPh 419
                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-711-417C-153
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417C
PRILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAS: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/238,212
FILING DATE: 02-YAX-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 470 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 153
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seg_documentation_block
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219 nValalaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys* 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 GAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCA 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 GlyTyrCysGlyArgSerTyrLysGlnArg***SerLeuGluGluHisLy 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660 AGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCACACTGT 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      710 ACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGACCTG 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   760 TGCAAGATAGGATCAGAGGATCTCTCGTGCTGGACAGACTAGCAAGTAA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                  260 CCTCGGGAGAAAATGAATGGCTCCCACAGGGACCAAGGCAGCTCGGCT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 TIGICGGGAGTIGGAGGCATTCGACTTCCTAACGGAAAACTAAAGTGTGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209
                                                                                                                                                                                                                                                                                                                                                           210 CTGTGAAATGAATGGGGAAGAATGTGCGGAGGATTTACGAATGCTTGATG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 CysLys1leGly***GluArgSerLeuValLeuAspArgLeuAlaSerAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           810 TGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         560 CCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCTCACAAATGT
                                                                                                                                                                                                                                                                                           160 GCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAATGGGCGTGC
                                                                                                                                                                                                                                                       to: 470
                                                                                                                                                           Percent Identity: 90.171
; SEQUENCE DESCRIPTION: Xea = any amino acid; SEQUENCE DESCRIPTION: SEQ ID NO: 153: US-08-711-417C-153
                                                                                                                           Length:
                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-711-417C-153 from: 1
                                                                                                                                                                                                   alignment_block:
US-08-711-417C-165 x US-08-711-417C-153
                                                                                                            alignment_scores:
Quality: 2202.50
Ratio: 5.087
Percent Similarity: 92.521
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APPLICANT: GEOTGOPOULOS, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
                                                                                    960 CCTGGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACGCCCCCGGGCGGTT 1009
                                                                                                                                           1010 CCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC...AGGCGC 1056
                                                                                                                                                                                                        1057 TCGGAGGCACCCCGCGCTCCAACCACTCGGCCCAGGACAGCGCCGTGGA 1106
236 **LeuSerAsp***ProTyrAspSerAla***TyrGluLysGlu***** 252
                            910 ATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGCCATCAACTA 959
                                              1107 GTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGGAGCGCGAGG 1156
                                                                                                                                                                                                                                                                                                                          1157 CGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAGGAGCAACAAC 1206
                                                                                                                                                                                                                                                                                                                                                                                   1207 GAGGAGCAGCGCAGCGGTCTTATCTACCTGACCAACCACATCGCCCGACG 1256
                                                                                                                                                              1304 TGCGCGCCGCCTCCGAGAACTCGCAGGACGCGCTCCGCGTGGTCAGCACC 1353
                                                                                                                                                                                                                                                                                  319 ****LeuLeuLeuLeuLeuSerLysAlaLys***Val***SerGluArgGluA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                              1257 CGCG...CAACGCGTGTCGCTCAAGGAGGAGCACCGCGCGCCTACGACCTGC 1303
                                                                                                                                                                                                                                                                                                                                          1354 AGCGGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCGGGTGCTCTT 1403
                                                                                                                                                                                                                                                                                                                                                                                                   1404 CCTGGATCACGTCATGTACACCATCCACATG......GGCTGCCACG 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1445 GCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCACAGCCAGGAC 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1495 CGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCGCTTCCACAT 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-711-417C-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 197, Application US/08711417C Patent No. 6228611 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1545 GAGC 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 *Ser 470
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51 CCCCCTGTAAGGGATACTCCAGATGAGGGCGATGAGCCCATGCCGATCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 CCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAAGCTCCAAGGGTGAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 TGGGCGTGCCTGTGAATGAATGGGGGAAGAATGTGCGGGGGATTTACGAA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 TGCTTGATGCCTCGGGAGAGAAATGAATGGCTCCCACAGGGACCAAGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AGCTCGGCTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT INEX. LISARCHEE
COMPUTER: IBM Compatible
CORRENT SYSTEM: Windows 95
SOFTWARE: FASTESO for Windows Version 2.0b
SOFTWARE: FASTESO for Windows Version 2.0b
SOFTWARE: FASTESO for Windows Version 2.0b
APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-Sep-1996
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/238,212
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-711-417C-197 from: 1 to: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 74.280
                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 10287/007001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-711-417C-197
                                                                                                                                                                                                                                                                                                         NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lignment_block:
US-08-711-417C-165 x US-08-711-417C-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 432 amino acids
           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 4.776
Percent Similarity: 78.887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 1963.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block
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1248 CGCCCGACGCGCGCAACGC...GTGTCGCTCAAGGAGGAGCACCGCGCCT 1294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1001 CGGGCGGTTCCGAGGTGCTCCGGTCATCAGCCCGATGTACCAGCTGCAC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1051 AGG...CGCTCGGAGGGCACCCCGCGCTCCAACCACTCGGCCCAGGACAG 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1098 CGCCGTGGAGTACCTGCTGCTCCTCCAAGGCCAAGTTGGTGCCCTCGG 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       951 CATCAACTACCTGGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACGCCCC 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 .AlavalAspAsnLeuLeuLeuLeuSerLysAlaLysSerValSerSerG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 alleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901 GAGAACGAAATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 801 AGCAAGTAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 ...... g 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              851 GGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAAG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTCGTGCTGGACAGACT 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 ......196
                                                                                                                                                                                                                                                                                                                                                        701 GCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCA 750
                                                                                                                                                                                                                                                                                                                              651 GGAACATAAAGAGGGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGG 700
                                                                                                                                                               551 GGAGGGACGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600
                                                                                                                                                                                                                                  601 CACAAATGIGGAIAIIGIGGCCGAAGCIAIAAACAGCGAACGICIIIAGA 650
                                                                                                                                                                                                                                                                                                   196 ......196
451 GGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCA 500
                                                                                                                         401 TICACAAAAGAAGCCACACIGGAGAACGGCCCTICCAGIGCAAICAGIGC 450
                                                                                                                                                                                                                                                                                                                                                                                                                       196
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Sequence 195, Application US/08711417C
Patent No. 6228611
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   1436 GCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGGTACCAC 1485
                                                  1295 ACGACCTGCTGCGCGCCGCCTCCGAGAACTCGCAGGACGCGCTCCGCGTG 1344
                                                                                                                  1345 GTCAGCACCAGCGGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCG 1394
                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-711-417C-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: Windows 95 SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY ACEA.

NAME: Myers, Louis P.

REGISTRATION NUMBER: 35,965

REFERENCE/FOOKET UNBER: 10287/007001

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 431 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO: 195:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 617/542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                  1536 CTTCCACATGAGC 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                     428 gTyrHisLeuSer 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
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51 CCCCCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGATCC 100 CCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAAGCTCCAAGAGTGAC 150 151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAAA 200 201 TGGGCGTGCCTGTGAATGAATGGGGAAGAATGTGCGGAGGATTTACGAA 250 251 TGCTTGATGCCTCGGGAGAAAATGAATGGCTCCCACAGGGACCAAGGC 300 301 AGCICGGCTITGICGGGAGTIGGAGGCAIICGACIICCIAACGGAAAACI 350 Align seg 1/1 to: US-08-711-417C-195 from: 1 to: 431 Gaps: 7 Length: SEQUENCE DESCRIPTION: SEQ ID NO: 195; 53 alignment_block: US-08-711-417C-165 x US-08-711-417C-195 4.703 Quality: 1923.50 53 Percent Similarity: Ratio: ; US-08-711-417C-195 51 ArgGlyMet alignment_scores: 101 53

1001 CGGGCGGTTCCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC 1050 951 CATCAACTACCTGGGGGCCGAGTCCCTGCGCCCGCTGGTGCAGACGCCCC 1000 1051 AGG...CGCTCGGAGGGCACCCCGCGCTCCAACCACTCGGCCCAGGACAG 1097 1098 GGCGGGGAGTACCTGCTGCTGCTCCCAAGGCCAAGTTGGTGCCCTCGG 1147 1148 AGCGCGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAG 1197 801 AGCAAGTAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTG 850 179 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 196 851 GGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAAG 900 1248 CGCCCGACGCGCGCAACGC...GTGTCGCTCAAGGAGGAGCACCGCGCCT 1294 1295 ACGACCTGCTGCGCCCCCTCCGAGAACTCGCAGGACGCGCTCCGCGTG 1344 1395 GGTGCTCTTCCTGGATCACGTCATGTACACCATCCACATG.......G 1435 1436 GCTGCCACGCCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCAC 1485 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 212 GAGAACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGC 950 1345 GTCAGCACCAGCGGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCG 1394 278 .AlaValAspAsnLeuLeuLeuLeuSerLysAlaLysSerValSerSerG 294 1486 AGCCAGGACCGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCG 1535 344 GAAGACCTGTGCAAGATAGGATCAGAGATCTCTCGTGCTGGACAGACT | :::|||:::|||327 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGluGlnArgAlaT 1536 CTTCCACATGAGC 1548 196 901

427 gTyrHisLeuSer 431
seq_name: /cgn2_6/ptodata/2/laa/6B_COMB.pep:US-08-711-417C-201
seq_documentation_block:
Sequence 201, Application US/08711417C

Patent No. 6228611 GENERAL INFORMATION:	
APPLICANT: Georgopoulos, Katia A. TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE	
NUMBER OF SEQUENCES: 202 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C.	
CITY: Boston STATE: MA	
COUNTRY: USA ZIP: 02110-2804 CONDITIED PERDARI.E FORM:	
COMPUTER VERSION COMPATIBLE COMPUTER: IBM Compatible	
FILING DATE: 03-Sep.1930 PRIOR APPLICATION DATE: 08/238,212	
FILING DATE: 02-MAY-1994 APPLICATION NUMBER: 08/121,438	
-1993 07/946,23	
FILING DATE: 14-SEP-1992 ATTORNEY/AGENT INFORMATION:	
P. : 35,9	
REFERENCE/DOCKET NUMBER: 10287/007001 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070	
TELEFAX: 617/542-8906	
INFORMATION FOR SEQ ID NO: 201: SEOURNCE CHARACTERISTICS:	
LENGTH: 334 amino acids TYPE: amino acid	
FRAGMENT TIFE: INCELLAR SEQUENCE DESCRIPTION: SEQ ID NO: 201: S-08-711-417C-201	
lianment scores:	
Percent Similarity: 188.830 Percent Identity: 88.830	
.lignment_block: US-08-711-417C-165 x US-08-711-417C-201	
Align seg 1/1 to: US-08-711-417C-201 from: 1 to: 334	
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471 GGGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAGCCCTTCA 520 	
521 AATGCCACTCTGCAACTACGCCTGCCGCGAGGACGCCCTCACTGGC 570 	
571 CACCTGAGGACGCACTCCGTTGGTAAACCTCACAAATGTGGATATTGTGG 620	
621 CCGAAGCTATAAACAGCGAACGTCTTTAGAGGAACATAAAGAGCGCTGCC 670	_

26		99
671	ACAACTACTTGGAAAGCATGGGCCTTCCGGGCACACTGTACCCAGTCATT	720
57	alil	28
721	AAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGACCTGTGCAAGATAGG 	770
771	ATCAGAGAGATCTCTCGTGCTGGACAGACTAGCAAGTAATGTCGCCAAAC 	820 92
821 92	GTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGGGCCTGTCCGAC 	870 108
871 109	ACGCCCTACGACAGTGCCACGTACGAGAGAGAGAACGAATGATGAAGTC	920
921	CCACGIGATGGACCAAGCCATCAACGCCATCAACTACCTGGGGGCCG	970
971	AGTCCCTGCGCCCGCTGGTGCAGACGCCCCCGGGCGGTTCCCGAGGTGGTC	1020 158
1021	CCGGTCATCAGCCCGATGTACCAGCTGCACAGGCGCTCGGAGGGCACCCC	1070 175
1071	GCGCTCCAACCACTCGGCCCAGGACAGCGCCGTGGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1120 192
1121	TCTCCAAGGCCAAGTTGGTGCCCTCGGAGCGCGAGCGTCCCCGAGCAAC	1170 208
1171	AGCTGCCAAGACTCCACGACACCGAGAGCAACAACGAGGAGCAGCGCAG	1220 225
1221	CGGTCTTATCTACCTGACCAACACACACGCCCGACGCGCGCAACGCGTGT 	1270 242
1271	CGCTCAAGGAGGAGCACCGGCCTACGACCTGCTGCGCGCCGCCTCCGAG	1320
1321	AACTCGCAGGACGCGCTCCGCGTGGTCAGCACCAGCGGGGAGCAGATCAA	1370
1371	GGTGTACAAGTGCGAACACTGCCGGGTGCTCTTCCTGGATCACGTCATGT	1420
1421	ACACCATCCACGTGGGCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAAC	308
1471 309	ATGTGCGGCTACCACAGCCAGGACGGTACGAGTTCTCGTCGCACATAAC	152(325
1521	. GCGAGGGAGCACCGCTTCCACATGAGC 1548	

us-08-711-417c-165.rai

Page 15

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APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 CCCCCCTGTAAGCGATACTCCAGATGAGGCGATGAGCCCATGCCGATCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                                           seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-711-417C-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-711-417C-199 from: 1 to: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 7
Percent Identity: 65.835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEEX: 200154
INFORMATION FOR SEQ ID NO: 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/238,212
FILING DATE: 02-YAX-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 199:
325 rArgGlyGluHisArgPheHisMetSer 334
                                                                                                  Sequence 199, Application US/08711417C Patent No. 6228611 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-711-417C-165 x US-08-711-417C-199
                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
Quality: 1681.00
Ratio: 4.556
Percent Similarity: 70.825
                                                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                    seq_documentation_block:
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15	1 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAAA	200
2	1 ArgGlyMet	
20	1 TGGGCGTGCCTGTGAAATGAATGGGGAAGAATGTGCGGAGGATTTACGAA	250
Ŋ	3 · · · · · · · · · · · · · · · · · · ·	53
25	1 TGCTTGATGCCTCGGGAGAGAAATGAATGGCTCCCACAGGGACCAAGGC	300
5	ε	53
30	1 AGCTCGGCTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACT	350
Ŋ	E	53
35	1 AAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGG	400
ις		53
40.	1 TTCACAAAAGAACCACACAGAGAAAGGGCCCTTCCAGTGCAATCAGTGC	450 63
45.	1 GGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCA	500
.020	1 TTCCGGGGGGGAGAACCCTTCAAATGCCACCTCTGCAACTACGCCTGCCGCCCCCCTTTTTTTT	550 97
25 6	1 GGAGGGACGCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT	109
09	1 CACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGA	650
10		109
65	1 GGAACATAAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGG	700
10	6	109
701	GCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCA	750 121
75.	1 GAAGACCTGTGCAAGATAGGATCAGAGAATCTCTCGTGCTGGACACT	800 138
13	1 AGCAAGTAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTG	850 155
15.	1 GGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGACAAG	900
90:	1 GAGAACGAAATGATGAAGTCCCAGGTGATGGACCAAGCCATCAACACGC	950 187
95	1 CATCAACTACCTGGGGCCGAGTCCCTGCGCCCGCTGGTGCAGACGCCCC	1000
100	1 CGGGCGGTTCCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC	1050

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APPLICANT: GEOrgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
1051 AGG...CGCTCGGAGGGCACCCCGCGCTCCAACCACTCGGCCCAGGACAG 1097
                                                                                                                       1098 CGCCGTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGG 1147
                                                                                                                                                                                                                                                  1148 AGCGCGAGGCGTCCCCGAGCACAGTGCCAAGACTCCACGGACACCGAG 1197
                                                                                                                                                                                                                                                                                                                                                                          1248 CGCCCGACGCGCGAACGC...GTGTCGCTCAAGGAGGAGCACCGCGCCT 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1295 ACGACCTGCTGCGCGCCGCCTCCGAGAACTCGCAGGACGCGCTCCGCGTG 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1345 GTCAGCACCAGCGGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCG 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1395 GGTGCTCTTCCTGGATCACGTCATGTACACCATCCACATG......G 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1436 GCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCAC 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1486 AGCCAGGACCGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCG 1535
                                221 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp. 236
                                                                                                                                                        237 .AlaValAspAsnLeuLeuLeuLeuSerLysAlaLysSerValSerSerG 253
                                                                                                                                                                                                                                                                                                                                                                                                          270 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIl 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-711-417C-200
                                                                                                                                                                                                                                                                                      253 luargGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :::|||:::||| | 286 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGluGlnArgAlaT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER INA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-Sep-1996
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
; Sequence 200, Application US/08711417C
; Patent No. 6226611
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1536 CTTCCACATGAGC 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:::|||:::|||
386 gTyrHisLeuSer 390
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STATE: MA
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101 CCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAAGCTCCAAGAGTGAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AGAGTCGTGGCCAGTAATGTTAAAGTAGACACTCAGAGTGATGAAGAGAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 TGGGCGTGCCTGTGAAATGAATGGGGAAGAATGTGCGGAGGATTTACGAA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 TGCTTGATGCCTCGGGAGAAATGAATGGCTCCCACAGGGACCAAGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AGCTCGGCTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 AAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 TTCACAAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 GGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501 ITCCGGGGAGAAGCCCTTCAAATGCCACCTCTGCAACTACGCCTGCCGCC 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 CCCCCCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGATCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 63.724
                ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8006
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLGGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 200:
APPLICATION NUMBER: 07/946,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 .....
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US-08-711-417C-165 x US-08-711-417C-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-711-417C-200
                                                                                                                                                                                                                                     LENGTH: 376 amino acids
                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 200: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 4.565
Percent Similarity: 68.330
                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 1625.00
                                                                                                                                                                                                                                                                                                                                                         US-08-711-417C-200
                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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AAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGA 65	ACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCA 750
140	OT CITATION TO THE PARTY OF THE
14	GAAATGATGAAGTCCACGTGATGGACCAAGCCATCAACACG ### Control of the cont
AGCTGTGCCAAGATAGGATCAGGAGATCTCTCGTGCTGGACAGACT 800 AAGTAATGTCGCCAAAGTCAGGAGATCTCTCGTGCTGGACAGACT 800 AAGTAATGTCGCCCAAAGTAAGAGCTCTATGCCTCAGAAATTTCTTG 850 III	### ATT AND THE FOR TH

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APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
1436 GCTGCCCACGGCTTCCGTCATCCTTTTGAGTGCAACATGTGCGGCTACCAC 1485
                                                                                          1486 AGCCAGGACCGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCG 1535
                                                                                                                  seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-711-417C-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110-2804
COMPUTER: RADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-711-417C-175 from: 1 to: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 236
Gaps: 1
Percent Identity: 97.881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/711,417C FILING DATE: 05-Sep-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 175: US-08-711-417C-175
                                                                                                                                                                                                                                                                                                                                        Sequence 175, Application US/08711417C; Patent No. 6228611; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-711-417C-165 x US-08-711-417C-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 175:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 1210.00
Ratio: 5.216
Percent Similarity: 98.305
                                                                                                                                                                                  1536 CTTCCACATGAGC 1548
                                                                                                                                                                                                            |:::|||:::|||
372 gTyrHisLeuSer 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
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850 GGGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAA 899

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1488 CCAGGACCGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCGCT 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1438 TGCCACGCCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCACAG 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1388 ACTGCCGGGTGCTCTTCCTGGATCACGTCATGTACACCATCCACATGGGC 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1338 CCGCGTGGTCAGCACCAGCGGGAGCAGATGAAGGTGTACAAGTGCGAAC 1387
                                                                                                                                                                     1000 CCGGCCGTTCCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCA 1049
                                                                                                                                                                                                                                 1050 CAGGCGCTCGGAGGGCACCCCGCGCTCCAACCACTCGGCCCAGGACAGCG 1099
                                                                                                                                                                                                                                                                                                                                                          GTGCCCTCGGAGCGCGTCCCCGAGCAACAGCTGCCAAGACTCCAC 1187
                                                                                                                                                                                                                                                                                                                                                                                                                     1188 GGACACCGAGAGCAACAAGGAGGAGCAGCGCAGCGGTCTTATCTACCTGA 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1238 CCAACCACATGGCCCGACGCGCAACGCGTGTCGCTCAAGGAGGAGCAC 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1288 CGCGCCTACGACCTGCTGCGCGCCGCCTCCGAGAACTCGCAGGACGCGCT 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 CysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHisSe 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 rGlnaspargTyrGluPheSerSerHisIleThrargGlyGluHisArgP 234
                                                                                                                                                                                                                                                                                                                                                                                                                                    950 CCATCAACTACCTGGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACGCCC 999
                                             900 GGAGAACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACG 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-711-417C-177
                                                                                                                                                                                     1 GlyAspLysGlyLeuSerAspThrProTyrAspSerAlaThrTyrGluLy 17
CCGTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: MA
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1097 GCGCCGTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCG 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1050 CAGG...CGCTCGGAGGGCACCCCGCGCTCCAACCACTCGGCCCAGGACA 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               850 GGGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAA 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        900 GGAGAACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACG 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              950 CCATCAACTACCTGGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACGCCC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sercent Identity: 97.899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 177:
US-08-711-417c-177
                                                                                                                                                                                                                                                                                                                   NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
                                                                                                                          PRIOR APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-711-417C-177 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-711-417C-165 x US-08-711-417C-177
                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                     COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 238 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 177: SEQUENCE CHARACTERISTICS:
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1...238
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 5.144
Percent Similarity: 97.899
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 1198.50
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
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1147	GAGCGGGGGGCGTCCCCGGAGCAACAGCTGCCAAGACTCCACGGACACCGA 	1196
117		1246 134
1247	TCGCCCACGCGCGCAACGCGTGTCGCTCAAGAGAGAACACCGCGCCC [1293 150
1294	TACGACCTGCTGCGCGCCTCCGAGAACTCGCAGGACGCGCTCCGCGT	13 4 3 167
1344	GGTCAGCACCAGCGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCC 	1393 184
1394	GGGTGCTCTTCCTGGATCACGTCATGTACACCATCCACATG	1434
1435	GGCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCA	1484 217

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